

ABSTRACT OF THE DISCLOSURE

A method for determining a target nucleic acid sequence is disclosed, wherein a preparation having a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence, is contacted with a blocking oligonucleotide complementary to at least a portion of the first region of dissimilar sequence of the non-target nucleic acid sequence, under conditions to hybridise the blocking oligonucleotide thereto and hybridized to the target nucleic acid sequence; and then sequenced such that the sequencing reaction proceeds into the second region of dissimilar sequence of the target nucleic acid sequence, whereby at least the second region of dissimilar sequence of the target nucleic acid sequence is determined; and wherein the sequencing reaction is blocked at least from proceeding into the second region of dissimilar sequence of the non-target nucleic acid sequence.